10/697,036

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=> d his

     (FILE 'HOME' ENTERED AT 15:42:50 ON 02 JUL 2007)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 15:43:53 ON 02 JUL 2007
L1            55 S OSMOSENSING (W) HISTIDINE (W) KINASE?
L2           135 S HYBRID(W)SENSOR (W)KINASE
L3             0 S L2(W)(LACK? OR DEFICIENT? OR MISS?)
L4             2 S L1 AND L2
L5            12 S CELL AND L1
L6             6 DUP REM L5 (6 DUPLICATES REMOVED)
L7            25 S (PLANT? OR BACTER?) AND L1
L8            11 DUP REM L7 (14 DUPLICATES REMOVED)
                 E NAKAJIMA H/AU
L9          9134 S E3
L10            1 S L1 AND L9

=>
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 NEWS  4  MAR 20  MARPAT now updated daily
 NEWS  5  MAR 22  LWPI reloaded
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 NEWS  8  APR 30  GENBANK reloaded and enhanced with Genome Project ID field
 NEWS  9  APR 30  CHEMCATS enhanced with 1.2 million new records
 NEWS 10  APR 30  CA/CAplus enhanced with 1870-1889 U.S. patent records
 NEWS 11  APR 30  INPADOC replaced by INPADOCDB on STN
 NEWS 12  MAY 01  New CAS web site launched
 NEWS 13  MAY 08  CA/CAplus Indian patent publication number format defined
 NEWS 14  MAY 14  RDISCLOSURE on STN Easy enhanced with new search and display
                  fields
 NEWS 15  MAY 21  BIOSIS reloaded and enhanced with archival data
 NEWS 16  MAY 21  TOXCENTER enhanced with BIOSIS reload
 NEWS 17  MAY 21  CA/CAplus enhanced with additional kind codes for German
                  patents
 NEWS 18  MAY 22  CA/CAplus enhanced with IPC reclassification in Japanese
                  patents
 NEWS 19  JUN 27  CA/CAplus enhanced with pre-1967 CAS Registry Numbers
 NEWS 20  JUN 29  STN Viewer now available
 NEWS 21  JUN 29  STN Express, Version 8.2, now available
 NEWS 22  JUL 02  LEMBASE coverage updated
 NEWS 23  JUL 02  LMEDLINE coverage updated
 NEWS 24  JUL 02  SCISEARCH enhanced with complete author names
 NEWS 25  JUL 02  CHEMCATS accession numbers revised
 NEWS 26  JUL 02  CA/CAplus enhanced with utility model patents from China

 NEWS EXPRESS  29 JUNE 2007:  CURRENT WINDOWS VERSION IS V8.2,
               CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
               AND CURRENT DISCOVER FILE IS DATED 4 MAY 2007.

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=> file medline embase biosis biotechds scisearch hcaplus ntis lifesci
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                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.42       0.42

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FILE 'LIFESCI' ENTERED AT 15:43:53 ON 02 JUL 2007
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=> s osmosensing (w) histidine (w) kinase?
L1          55 OSMOSENSING (W) HISTIDINE (W) KINASE?

=> s hybrid(w)sensor (w)kinase
L2         135 HYBRID(W) SENSOR (W) KINASE

=> s l2(w)(lack? or deficient? or miss?)
L3           0 L2(W)(LACK? OR DEFICIENT? OR MISS?)

=> s l1 and l2
L4           2 L1 AND L2

=> d 1-2 ibib ab

L4    ANSWER 1 OF 2  BIOTECHDS COPYRIGHT 2007 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2004-15129  BIOTECHDS
TITLE:            New transformed cell in which a polynucleotide coding for
                  osmosensing histidine kinase
                  having no transmembrane region has been introduced, useful
                  for identifying an antifungal compound useful for killing a
                  fungus;
                     vector expression in host cell for use in drug screening
                     and fungus infection therapy
AUTHOR:           NAKAJIMA H
PATENT ASSIGNEE:  SUMITOMO CHEM CO LTD
PATENT INFO:      EP 1415996 6 May 2004
APPLICATION INFO: EP 2003-256895 30 Oct 2003
PRIORITY INFO:    JP 2002-317736 31 Oct 2002; JP 2002-317736 31 Oct 2002
```

DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2004-341880 [32]

AB DERWENT ABSTRACT:

NOVELTY - A transformed cell in which a polynucleotide having a sequence encoding an amino acid sequence of an osmosensing histidine kinase having no transmembrane region has been introduced in a functional form into a cell deficient in at least one hybrid-sensor kinase, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for: (1) assaying the antifungal activity of a substance; (2) identifying an antifungal compound; (3) an antifungal compound selected by the method above; (4) killing a fungus; (5) an osmosensing histidine kinase having no transmembrane region and derived from a plant-pathogenic filamentous fungus or which has an amino acid sequence selected from: (a) a sequence of 1293, 1307 or 1438 amino acids (SEQ ID NO: 41, 55 or 68) given in the specification or a sequence 95% or more homologous to SEQ ID NO: 41, 55 or 68; (b) a sequence encoded by a DNA amplified by PCR using a Fusarium oxysporum-derived cDNA as a template and using oligonucleotides having the nucleotide sequences tgcactagtatggttgacgacgcggccctcgc (SEQ ID NO: 52) and gagctgcagttagttggtaagacttcgcatatc (SEQ ID NO: 53) as primers;(c) a sequence encoded by a DNA amplified by PCR using Mycospharella tritici-derived cDNA as a template and using oligonucleotides having the sequences cccactagtatgctgcaagaagagacttcg (SEQ ID NO: 64) and cctaagcttctcagctgctatgggcacgaa (SEQ ID NO: 65) as primers; (d) a sequence encoded by a DNA amplified by PCR using Thanapethorus cucumeris-derived cDNA as a template and using oligonucleotides having the sequences ggaactagtatggcaggtacaacgggggacacc (SEQ ID NO: 85) and tgcaagcttttagtgggcaccgtggggtgttacg (SEQ ID NO: 86) as primers; and (e) a sequence derived from Phytophthora infestans and has the amino acid sequence of 124 amino acids (SEQ ID NO: 90) given in the specification; (6) a polynucleotide having a nucleotide sequence encoding an amino acid sequence of an osmosensing histidine kinase having no transmembrane region derived from a plant-pathogen filamentous fungus described above or having a sequence of 3882, 3924, or 4317 bp (SEQ ID NO: 42, 56, or 69) given in the specification; (7) obtaining the polynucleotide above; and (8) an oligonucleotide which comprises a nucleotide sequence selected from 17 sequences of 23-34 bp (SEQ ID NO: 30-40, 52, 53, 64, 65, 85, and 86) given in the specification, e.g., aacatgtcccacgarattcgmacacc (SEQ ID NO: 30) caccgagattcgvacacccatgaaygg (SEQ ID NO: 31) aggccttccaaaaggctctvcggga (SEQ ID NO: 32) gagatggaccctgaaatcacmac (SEQ ID NO: 33) cagatattctcyagygaagtytckcg (SEQ ID NO: 34) atagcrttgccaacmaggttmagaataa (SEQ ID NO: 35) aacttgatggcrttkccaacmaggtt (SEQ ID NO: 36) ctctgtgaacttgatrgcrttkccaac (SEQ ID NO: 37) atacacttttcncggtcacccatcat (SEQ ID NO: 38) tccatctgbgcctggatacacttttc (SEQ ID NO: 39) ggcttvgavagatactcgtccatctg (SEQ ID NO: 40).

BIOTECHNOLOGY - Preferred Transformed Cell: The polynucleotide is a polynucleotide complementing the deficiency in hybrid-sensor kinase in the cell deficient in at least one hybrid-sensor kinase in which the polynucleotide has been introduced. The cell is a microorganism, particularly budding yeast. The osmosensing histidine kinase having no transmembrane region is an osmosensing histidine kinase having no transmembrane region and having a mutation which confers resistance to any of a dicarboxylimide antifungal compound, an aromatic hydrocarbon antifungal compound and a phenylpyrrole antifungal compound to the cell. The osmosensing histidine kinase is derived from a plant-pathogenic filamentous fungus and has no transmembrane region. The osmosensing histidine kinase has an amino acid sequence of 1315, 1307, 1293, 1307, 1438 or 124 amino acids (SEQ ID NO: 1, 16, 41, 55, 68 or 90, respectively) given in the specification.

The nucleotide sequence encoding an amino acid sequence of the osmosensing histidine kinase is a sequence of 3948, 3924, 3882, 3924, or 4317 bp (SEQ ID NO: 2, 17, 42, 56, or 69, respectively) also given in the specification. Preferred Method: Assaying the antifungal activity of a substance comprises culturing a transformed cell defined above in the presence of a test substance, measuring an amount of intracellular signal transduction from the osmosensing histidine kinase having no transmembrane region expressed in the cultured transformed cell or an index value having the correlation, and assessing the antifungal activity of the test substance based on a difference between an amount of intracellular signal transduction or an index value having the correlation measured and a control. The amount of intracellular signal transduction or the index value having the correlation is an amount of growth of the transformed cell. Identifying an antifungal compound comprises selecting an antifungal compound based on the antifungal activity assessed in the assaying method defined above. Killing a fungus comprises identifying an antifungal compound by the method above and contacting the fungus with the identified antifungal compound. Obtaining the polynucleotide above comprises amplifying a desired polynucleotide by PCR using the oligonucleotide above and recovering the amplified desired polynucleotide.

ACTIVITY - Fungicide. No biological data given.

MECHANISM OF ACTION - None given.

USE - The transformed cell is useful for assaying the antifungal activity of a substance and identifying an antifungal compound which is useful for killing a fungus (claimed).

EXAMPLE - BcOS-1 DNA was cloned into a shuttle vector p415ADH (ATCC87312) replicable in yeast and Escherichia coli. Both were digested, separated by agarose gel electrophoresis, and a part of the gel containing a desired DNA was excised. The BcOS-1 DNA was inserted between SpeI and PstI sites in the multicloning site of the shuttle vector. A nucleotide sequence of the resulting expression plasmid was analyzed after a sequencing reaction. The nucleotide sequence of 3948 bp (SEQ ID NO: 2) given in the specification was obtained and it was confirmed that the expression plasmid pADHBcOS1 harbored a DNA having a nucleotide sequence encoding an amino acid sequence of BcOS-1. The prepared expression plasmid was introduced into each of budding yeast (Saccharomyces cerevisiae AH22 strain) (IFO10144) and TM182 strain. By utilizing disappearance of leucine auxotrophy in the resulting transformed budding yeast, the transformed budding yeast AH22 strain was selected on a Glu-Leu agar medium, and the transformed budding yeast TM182 was selected on a Gal-Ura-Leu agar medium. It was confirmed that the resulting TM182-BcOS1 grows even when transplanted to a Glu-Ura-Leu medium. (211 pages)

L4 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER:	2004:370684 HCAPLUS
DOCUMENT NUMBER:	140:369919
TITLE:	Transformed cell with enhanced sensitivity to antifungal compound, expressing mutated gene, os-1, for an osmosensing histidine kinase, and uses for fungicide screening
INVENTOR(S):	Nakajima, Hiroki
PATENT ASSIGNEE(S):	Sumitomo Chemical Company, Limited, Japan
SOURCE:	Eur. Pat. Appl., 211 pp. CODEN: EPXXDW
DOCUMENT TYPE:	Patent
LANGUAGE:	English
FAMILY ACC. NUM. COUNT:	1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

```
     EP 1415996            A2    20040506    EP 2003-256895          20031030
     EP 1415996            A3    20040901
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
     JP 2005087182         A     20050407    JP 2003-354761          20031015
     SG 127705             A1    20061229    SG 2003-6525            20031030
     US 2004137594         A1    20040715    US 2003-697036          20031031
PRIORITY APPLN. INFO.:                       JP 2002-317736       A  20021031
                                             JP 2003-207458       A  20030813
AB   An object of the present invention is to provide a method of detecting the
     antifungal activity and a method of antifungal screening using filamentous
     fungi homologs of Neurispora crassa os-1 gene encoding a two-component
     system osmosensing histidine kinase having
     no transmembrane region.  OS-1 protein and cDNA sequences from
     phytopathogenic fungi, including Botryotinia fuckeliana (BcOS-1),
     Magnaoirthe grisea (HIK1), Fusarium oxysporum (FoOS-1), Mycosphaerella
     tritici (StOS-1), Thanatephorus cucumeris (RsOS-1), and Phytophthora
     infestans (PiOS-1), are provided.  The present invention provides
     transformed cells (such as budding yeast) in which a os-1 gene homolog
     encoding an osmosensing histidine kinase
     having no transmembrane region has been introduced in a functional form
     into a cell deficient in at least one hybrid-sensor
     kinase.  The os-1 transgene is carrying a mutation which confers
     resistance to the cell to any of a dicarboxyimide antifungal compound, an
     aromatic hydrocarbon antifungal compound and a phenylpyrrole antifungal
compound
     Provided are a method of assaying the antifungal activity of a test
     substance using the transformed cell, and a method of identifying an
     antifungal compound


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     (FILE 'HOME' ENTERED AT 15:42:50 ON 02 JUL 2007)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 15:43:53 ON 02 JUL 2007
L1            55 S OSMOSENSING (W) HISTIDINE (W) KINASE?
L2           135 S HYBRID(W)SENSOR (W)KINASE
L3             0 S L2(W)(LACK? OR DEFICIENT? OR MISS?)
L4             2 S L1 AND L2

=> s cell and l1
L5            12 CELL AND L1

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6             6 DUP REM L5 (6 DUPLICATES REMOVED)

=> d 1-6 ibib ab

L6   ANSWER 1 OF 6  HCAPLUS  COPYRIGHT 2007 ACS on STN
ACCESSION NUMBER:         2006:184567  HCAPLUS
DOCUMENT NUMBER:          145:24003
TITLE:                    Comparative genomics of the HOG-signalling system in
                          fungi
AUTHOR(S):                Krantz, Marcus; Becit, Evren; Hohmann, Stefan
CORPORATE SOURCE:         Department for Cell and Molecular Biology, Goeteborg
                          University, Goeteborg, 40530, Swed.
SOURCE:                   Current Genetics (2006), 49(3), 137-151
                          CODEN: CUGED5; ISSN: 0172-8083
PUBLISHER:                Springer
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
```

AB Signal transduction pathways play crucial roles in cellular adaptation to environmental changes. In this study, we employed comparative genomics to analyze the high osmolarity glycerol pathway in fungi. This system contains several signaling modules that are used throughout eukaryotic evolution, such as a mitogen-activated protein kinase and a phosphorelay module. Here we describe the identification of pathway components in 20 fungal species. Although certain proteins proved difficult to identify due to low sequence conservation, a main limitation was incomplete, low coverage genomic sequences and fragmentary genome annotation. Still, the pathway was readily reconstructed in each species, and its architecture could be compared. The most striking difference concerned the Sho1 branch, which frequently does not appear to activate the Hog1 MAPK module, although its components are conserved in all but one species. In addition, two species lacked apparent orthologs for the Sln1 osmosensing histidine kinase. All information gathered has been compiled in an MS Excel sheet, which also contains interactive visualization tools. In addition to primary sequence anal., we employed anal. of protein size conservation. Protein size appears to be conserved largely independently from primary sequence and thus provides an addnl. tool for functional anal. and ortholog identification.
REFERENCE COUNT: 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 6 BIOTECHDS COPYRIGHT 2007 THE THOMSON CORP. on STN
DUPLICATE 1
ACCESSION NUMBER: 2004-15129 BIOTECHDS
TITLE: New transformed cell in which a polynucleotide coding for osmosensing histidine kinase having no transmembrane region has been introduced, useful for identifying an antifungal compound useful for killing a fungus;
vector expression in host cell for use in drug screening and fungus infection therapy
AUTHOR: NAKAJIMA H
PATENT ASSIGNEE: SUMITOMO CHEM CO LTD
PATENT INFO: EP 1415996 6 May 2004
APPLICATION INFO: EP 2003-256895 30 Oct 2003
PRIORITY INFO: JP 2002-317736 31 Oct 2002; JP 2002-317736 31 Oct 2002
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2004-341880 [32]
AB DERWENT ABSTRACT:
NOVELTY - A transformed cell in which a polynucleotide having a sequence encoding an amino acid sequence of an osmosensing histidine kinase having no transmembrane region has been introduced in a functional form into a cell deficient in at least one hybrid-sensor kinase, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for: (1) assaying the antifungal activity of a substance; (2) identifying an antifungal compound; (3) an antifungal compound selected by the method above; (4) killing a fungus; (5) an osmosensing histidine kinase having no transmembrane region and derived from a plant-pathogenic filamentous fungus or which has an amino acid sequence selected from: (a) a sequence of 1293, 1307 or 1438 amino acids (SEQ ID NO: 41, 55 or 68) given in the specification or a sequence 95% or more homologous to SEQ ID NO: 41, 55 or 68; (b) a sequence encoded by a DNA amplified by PCR using a Fusarium oxysporum-derived cDNA as a template and using oligonucleotides having the nucleotide sequences tgcactagtatggttgacgacgcggccctcgc (SEQ ID NO: 52) and gagctgcagttagttggtaagacttcgcatatc (SEQ ID NO: 53) as primers;(c) a sequence encoded by a DNA amplified by PCR using Mycospharella tritici-derived cDNA as a template and using oligonucleotides having the sequences cccactagtatgctgcaagaagagacttcg (SEQ ID NO: 64) and cctaagcttctcagctgctatgggcacgaa (SEQ ID NO: 65) as primers; (d) a sequence

encoded by a DNA amplified by PCR using Thanapethorus cucumeris-derived cDNA as a template and using oligonucleotides having the sequences ggaactagtatggcaggtacaacgggggacacc (SEQ ID NO: 85) and tgcaagcttttagtgggcaccgtggggtgttacg (SEQ ID NO: 86) as primers; and (e) a sequence derived from Phytophthora infestans and has the amino acid sequence of 124 amino acids (SEQ ID NO: 90) given in the specification; (6) a polynucleotide having a nucleotide sequence encoding an amino acid sequence of an osmosensing histidine kinase having no transmembrane region derived from a plant-pathogen filamentous fungus described above or having a sequence of 3882, 3924, or 4317 bp (SEQ ID NO: 42, 56, or 69) given in the specification; (7) obtaining the polynucleotide above; and (8) an oligonucleotide which comprises a nucleotide sequence selected from 17 sequences of 23-34 bp (SEQ ID NO: 30-40, 52, 53, 64, 65, 85, and 86) given in the specification, e.g., aacatgtcccacgarattcgmacacc (SEQ ID NO: 30) caccgagattcgvacacccatgaaygg (SEQ ID NO: 31) aggccttccaaaaggctctvcggga (SEQ ID NO: 32) gagatggaccctgaaatcacmac (SEQ ID NO: 33) cagatattctcyagygaagtytckcg (SEQ ID NO: 34) atagcrttgccaacmaggttmagaataa (SEQ ID NO: 35) aacttgatggcrttkccaacmaggtt (SEQ ID NO: 36) ctctgtgaacttgatrgcrttkccaac (SEQ ID NO: 37) atacacttttcncggtcacccatcat (SEQ ID NO: 38) tccatctgbgcctggatacacttttc (SEQ ID NO: 39) ggcttvgavagatactcgtccatctg (SEQ ID NO: 40).

BIOTECHNOLOGY - Preferred Transformed Cell: The polynucleotide is a polynucleotide complementing the deficiency in hybrid-sensor kinase in the cell deficient in at least one hybrid-sensor kinase in which the polynucleotide has been introduced. The cell is a microorganism, particularly budding yeast. The osmosensing histidine kinase having no transmembrane region is an osmosensing histidine kinase having no transmembrane region and having a mutation which confers resistance to any of a dicarboxylimide antifungal compound, an aromatic hydrocarbon antifungal compound and a phenylpyrrole antifungal compound to the cell. The osmosensing histidine kinase is derived from a plant-pathogenic filamentous fungus and has no transmembrane region. The osmosensing histidine kinase has an amino acid sequence of 1315, 1307, 1293, 1307, 1438 or 124 amino acids (SEQ ID NO: 1, 16, 41, 55, 68 or 90, respectively) given in the specification. The nucleotide sequence encoding an amino acid sequence of the osmosensing histidine kinase is a sequence of 3948, 3924, 3882, 3924, or 4317 bp (SEQ ID NO: 2, 17, 42, 56, or 69, respectively) also given in the specification. Preferred Method: Assaying the antifungal activity of a substance comprises culturing a transformed cell defined above in the presence of a test substance, measuring an amount of intracellular signal transduction from the osmosensing histidine kinase having no transmembrane region expressed in the cultured transformed cell or an index value having the correlation, and assessing the antifungal activity of the test substance based on a difference between an amount of intracellular signal transduction or an index value having the correlation measured and a control. The amount of intracellular signal transduction or the index value having the correlation is an amount of growth of the transformed cell. Identifying an antifungal compound comprises selecting an antifungal compound based on the antifungal activity assessed in the assaying method defined above. Killing a fungus comprises identifying an antifungal compound by the method above and contacting the fungus with the identified antifungal compound. Obtaining the polynucleotide above comprises amplifying a desired polynucleotide by PCR using the oligonucleotide above and recovering the amplified desired polynucleotide.

ACTIVITY - Fungicide. No biological data given.

MECHANISM OF ACTION - None given.

USE - The transformed cell is useful for assaying the antifungal activity of a substance and identifying an antifungal compound

which is useful for killing a fungus (claimed).

EXAMPLE - BcOS-1 DNA was cloned into a shuttle vector p415ADH (ATCC87312) replicable in yeast and Escherichia coli. Both were digested, separated by agarose gel electrophoresis, and a part of the gel containing a desired DNA was excised. The BcOS-1 DNA was inserted between SpeI and PstI sites in the multicloning site of the shuttle vector. A nucleotide sequence of the resulting expression plasmid was analyzed after a sequencing reaction. The nucleotide sequence of 3948 bp (SEQ ID NO: 2) given in the specification was obtained and it was confirmed that the expression plasmid pADHBcOS1 harbored a DNA having a nucleotide sequence encoding an amino acid sequence of BcOS-1. The prepared expression plasmid was introduced into each of budding yeast (Saccharomyces cerevisiae AH22 strain) (IFO10144) and TM182 strain. By utilizing disappearance of leucine auxotrophy in the resulting transformed budding yeast, the transformed budding yeast AH22 strain was selected on a Glu-Leu agar medium, and the transformed budding yeast TM182 was selected on a Gal-Ura-Leu agar medium. It was confirmed that the resulting TM182-BcOS1 grows even when transplanted to a Glu-Ura-Leu medium. (211 pages)

L6 ANSWER 3 OF 6 MEDLINE on STN

ACCESSION NUMBER: 2003280893 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12672798
TITLE: Analysis of the role of the EnvZ linker region in signal transduction using a chimeric Tar/EnvZ receptor protein, Tez1.
AUTHOR: Zhu Yan; Inouye Masayori
CORPORATE SOURCE: Department of Biochemistry, Robert Wood Johnson Medical School, Piscataway, New Jersey 08854, USA.
CONTRACT NUMBER: GM19043 (NIGMS)
SOURCE: The Journal of biological chemistry, (2003 Jun 20) Vol. 278, No. 25, pp. 22812-9. Electronic Publication: 2003-04-02.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE) (RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200308
ENTRY DATE: Entered STN: 17 Jun 2003
Last Updated on STN: 22 Aug 2003
Entered Medline: 21 Aug 2003

AB Tez1 is a chimeric protein in which the periplasmic and transmembrane domains of Tar, a chemosensor, are fused to the cytoplasmic catalytic domain of EnvZ, an osmosensing histidine kinase, through the EnvZ linker. Unlike Taz1 (a similar hybrid with the Tar linker), Tez1 could not respond to Tar ligand, aspartate, whereas single Ala insertion at the transmembrane/linker junction, as seen in Tez1A1, restored the aspartate-regulatable phenotype. Analysis of the Ala insertion site requirement and the nature of the insertion residue on the phenotype of Tez1 indicated that a junction region between the transmembrane domain and the predicted helix I in the linker is critical to signal transduction. Random mutagenesis revealed that P185Q mutation in the Tez1 linker restored the aspartate-regulatable phenotype. Substitution mutations at Pro-185 further demonstrated that specific residues are required at this site for an aspartate response. None of the hybrid receptors constructed with different Tar/EnvZ fusion sites in the linker could respond to aspartate, suggesting that specific interactions between the two predicted helices in the linker are important for the linker function. In addition, a mutation (F220D) known to cause an OmpCc phenotype in EnvZ resulted in similar OmpCc phenotypes in both Tez1A1 and Tez1, indicating the importance of the predicted helix II in signal propagation. Together, we propose that the N-terminal junction region

modulates the alignment between the two helices in the linker upon signal input. In turn helix II propagates the resultant conformational signal into the downstream catalytic domain of EnvZ to regulate its bifunctional enzymatic activities.

L6 ANSWER 4 OF 6 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2000:265981 BIOSIS
DOCUMENT NUMBER: PREV200000265981
TITLE: A monomeric histidine kinase derived from EnvZ, an Escherichia coli osmosensor.
AUTHOR(S): Qin, Ling; Dutta, Rinku; Kurokawa, Hirofumi; Ikura, Mitsuhiko; Inouye, Masayori [Reprint author]
CORPORATE SOURCE: Department of Biochemistry, UMDNJ, Robert Wood Johnson Medical School, 675 Hoes Lane, Piscataway, NJ, 08854, USA
SOURCE: Molecular Microbiology, (April, 2000) Vol. 36, No. 1, pp. 24-32. print.
CODEN: MOMIEE. ISSN: 0950-382X.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 30 Jun 2000
Last Updated on STN: 5 Jan 2002

AB Histidine kinases function as dimers. The kinase domain of the osmosensing histidine kinase EnvZ of Escherichia coli consists of two domains: domain A (67 residues) responsible for histidine phosphotransfer and dimerization, and domain B (161 residues) responsible for the catalytic and ATP-binding function. The individual structures of these two domains have been recently solved by NMR spectroscopy. Here, we demonstrate that an enzymatically functional monomeric histidine kinase can be constructed by fusing in tandem two domains A and one domain B to produce a single polypeptide (A-A-B). We show that this protein, EnvZc(AAB), is soluble and exists as a stable monomer. The autophosphorylation and OmpR kinase activities of the monomeric EnvZc(AAB) are similar to that of the wild-type EnvZ, while OmpR-binding and phosphatase functions are reduced. V8 protease digestion and mutational analyses indicate that His-243 of only the amino proximal domain A is phosphorylated. Based on these results, molecular models are proposed for the structures of EnvZc(AAB) and the kinase domain of EnvZ. The present results demonstrate for the first time the construction of a functional, monomeric histidine kinase, further structural studies of which may provide important insights into the structure-function relationships of histidine kinases.

L6 ANSWER 5 OF 6 BIOTECHDS COPYRIGHT 2007 THE THOMSON CORP. on STN
ACCESSION NUMBER: 1999-13321 BIOTECHDS
TITLE: Osmosensing histidine-kinases, useful for screening for fungicide compounds and for the development of fungicide compounds; Candida albicans, Neurospora crassa and Saccharomyces cerevisiae recombinant osmosensing thymidine-kinase, useful for drug screening for fungicide
AUTHOR: Alex L A; Simon M I; Selitrennikoff C; Agnan J
PATENT ASSIGNEE: Univ.Technol.Corp.; California-Inst.Technol.
LOCATION: Boulder, CO, USA; CA, USA.
PATENT INFO: US 5939306 17 Aug 1999
APPLICATION INFO: US 1997-843530 16 Apr 1997
PRIORITY INFO: US 1997-843530 16 Apr 1997
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1999-468407 [39]

AB A purified and isolated DNA sequence (I) encoding an osmosensing histidine-kinase (II) (EC-2.7.1.21), along with vectors and host cells harboring (I) and its variants are new. (I) Is from Candida albicans, Neurospora crassa or Saccharomyces cerevisiae, and the preferred host cell for the production of (II) is C.

albicans. The histidine-kinase is useful in drug screening for fungicides as well as for fungicide drug development. In an example, N. crassa was transfected with plasmid pMMS100 which was found to encode (II). (110pp)

L6 ANSWER 6 OF 6 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 97287887 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9142740
TITLE: The osmotic-1 locus of Neurospora crassa encodes a putative histidine kinase similar to osmosensors of bacteria and yeast.
AUTHOR: Schumacher M M; Enderlin C S; Selitrennikoff C P
CORPORATE SOURCE: University of Colorado Health Sciences Center, B-111, 4200 East 9th Avenue, Denver, CO 80262, USA.
CONTRACT NUMBER: R01:AI33354-02 (NIAID)
SOURCE: Current microbiology, (1997 Jun) Vol. 34, No. 6, pp. 340-7. Journal code: 7808448. ISSN: 0343-8651.
PUB. COUNTRY: United States
DOCUMENT TYPE: (COMPARATIVE STUDY) Journal; Article; (JOURNAL ARTICLE) (RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Biotechnology
OTHER SOURCE: GENBANK-U53189
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 16 Jul 1997
Last Updated on STN: 16 Jul 1997
Entered Medline: 30 Jun 1997

AB Osmotically sensitive mutants of Neurospora crassa are unable to grow on medium supplemented with 4% NaCl, have altered morphologies and cell-wall compositions, and are resistant to dicarboximide fungicides. Osmotic-1 (os-1) mutants have a unique characteristic of forming protoplasts that grow and divide in specialized liquid medium, suggesting that the os-1+ gene product is important for cell -wall assembly. A cosmid containing the os-1+ locus of N. crassa, isolated from a genomic cosmid library by chromosomal walk from a closely linked gene, was used to subclone the os-1+ gene by functional complementation of an os-1 mutant. Analysis of the sequence of complementing DNA predicts that os-1+ encodes a predicted protein similar to sensor-histidine kinases of bacteria and a yeast osmosensor-histidine kinase. Importantly, the predicted os-1+ protein is identical to the N. crassa nik-1 predicted protein that was identified by using polymerase chain reaction primers directed against histidine kinase consensus DNA sequences. Our results indicate that nik-1 and os-1 encode the same osmosensing histidine kinase that plays an important role in the regulation of cell-wall assembly and, probably, other cell responses to changes in external osmolarity.

=> d his

(FILE 'HOME' ENTERED AT 15:42:50 ON 02 JUL 2007)

FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS, LIFESCI' ENTERED AT 15:43:53 ON 02 JUL 2007

L1 55 S OSMOSENSING (W) HISTIDINE (W) KINASE?
L2 135 S HYBRID(W)SENSOR (W)KINASE
L3 0 S L2(W)(LACK? OR DEFICIENT? OR MISS?)
L4 2 S L1 AND L2
L5 12 S CELL AND L1
L6 6 DUP REM L5 (6 DUPLICATES REMOVED)

=> s (plant? or bacter?) and l1

L7 25 (PLANT? OR BACTER?) AND L1

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8 11 DUP REM L7 (14 DUPLICATES REMOVED)

=> d 1-11 ibib ab

L8 ANSWER 1 OF 11 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2006:285558 BIOSIS
DOCUMENT NUMBER: PREV200600282664
TITLE: Comparative genomics of the HOG-signalling system in fungi.
AUTHOR(S): Krantz, Marcus; Becit, Evren; Hohmann, Stefan [Reprint Author]
CORPORATE SOURCE: Univ Gothenburg, Dept Cell and Mol Biol, Box 462, S-40530 Gothenburg, Sweden
hohmann@gmm.gu.se
SOURCE: Current Genetics, (MAR 2006) Vol. 49, No. 3, pp. 137-151.
CODEN: CUGED5. ISSN: 0172-8083.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 24 May 2006
Last Updated on STN: 24 May 2006
AB Signal transduction pathways play crucial roles in cellular adaptation to environmental changes. In this study, we employed comparative genomics to analyse the high osmolarity glycerol pathway in fungi. This system contains several signalling modules that are used throughout eukaryotic evolution, such as a mitogen-activated protein kinase and a phosphorelay module. Here we describe the identification of pathway components in 20 fungal species. Although certain proteins proved difficult to identify due to low sequence conservation, a main limitation was incomplete, low coverage genomic sequences and fragmentary genome annotation. Still, the pathway was readily reconstructed in each species, and its architecture could be compared. The most striking difference concerned the Sho1 branch, which frequently does not appear to activate the Hog1 MAPK module, although its components are conserved in all but one species. In addition, two species lacked apparent orthologues for the Sln1 osmosensing histidine kinase. All information gathered has been compiled in an MS Excel sheet, which also contains interactive visualisation tools. In addition to primary sequence analysis, we employed analysis of protein size conservation. Protein size appears to be conserved largely independently from primary sequence and thus provides an additional tool for functional analysis and orthologue identification.

L8 ANSWER 2 OF 11 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
ACCESSION NUMBER: 2006:250002 BIOSIS
DOCUMENT NUMBER: PREV200600250028
TITLE: Survey of mutations of a histidine kinase gene Bc0S1 in dicarboximide-resistant field isolates of Botrytis cinerea.
AUTHOR(S): Oshima, Michiyo; Banno, Shinpei; Okada, Kiyotsugu; Takeuchi, Taeko; Kimura, Makoto; Ichiishi, Akihiko; Yamaguchi, Isamu; Fujimura, Makoto [Reprint Author]
CORPORATE SOURCE: Toyo Univ, Fac Life Sci, Gunma 3740193, Japan
fujmura@itakura.toyo.ac.jp
SOURCE: Journal of General Plant Pathology, (FEB 2006) Vol. 72, No. 1, pp. 65-73.
ISSN: 1345-2630.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 26 Apr 2006
Last Updated on STN: 26 Apr 2006
AB Previously, we cloned a putative osmosensing histidine kinase gene (BcOS1) and revealed that a single amino acid

substitution, isoleucine to serine at codon 365, conferred dicarboximide resistance in field isolates of Botrytis cinerea. This point mutation (type I) occurred within the restriction enzyme TaqI site of the wild-type BcOS1 gene. Thus, a procedure was developed for detecting the type I mutation of the BcOS1 gene using a polymerase chain reaction (PCR) in combination with restriction fragment-length polymorphism (RFLP). Diagnosis by PCR-RFLP was conducted on the 105 isolates isolated from 26 fields in Japan. All dicarboximide-sensitive isolates (49 isolates) had the wild-type BcOS1 gene, and the 43 isolates with the type I mutation were resistant to dicarboximides without exception. These data indicate that dicarboximide-resistant isolates with type I mutation are widespread throughout Japan. However, other types of dicarboximide resistance were detected among isolates from Osaka; among the 24 resistant isolates from Osaka, 12 had the BcOS1 gene without the type I mutation. BcOS1 gene sequencing of these resistant isolates classified them into two groups, type II and type III. The type II isolates have three amino acid substitutions within BcOS1p ((368)Val to Phe, (369)Gln to His, and (447)Thr to Ser). The type III isolates have two amino acid substitutions within BcOS1p ((369)Gln to Pro and (373)Asn to Ser). These amino acid changes are located on the amino acid repeat domain in BcOS1p. The three types of resistant isolates were all moderately resistant to dicarboximides without significant osmotic sensitivity, and their pathogenicity on cucumber leaves was also very similar to that of the wild-type isolate.

L8 ANSWER 3 OF 11 BIOTECHDS COPYRIGHT 2007 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2004-15129 BIOTECHDS
TITLE: New transformed cell in which a polynucleotide coding for osmosensing histidine kinase having no transmembrane region has been introduced, useful for identifying an antifungal compound useful for killing a fungus;
vector expression in host cell for use in drug screening and fungus infection therapy
AUTHOR: NAKAJIMA H
PATENT ASSIGNEE: SUMITOMO CHEM CO LTD
PATENT INFO: EP 1415996 6 May 2004
APPLICATION INFO: EP 2003-256895 30 Oct 2003
PRIORITY INFO: JP 2002-317736 31 Oct 2002; JP 2002-317736 31 Oct 2002
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2004-341880 [32]
AB DERWENT ABSTRACT:
NOVELTY - A transformed cell in which a polynucleotide having a sequence encoding an amino acid sequence of an osmosensing histidine kinase having no transmembrane region has been introduced in a functional form into a cell deficient in at least one hybrid-sensor kinase, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for: (1) assaying the antifungal activity of a substance; (2) identifying an antifungal compound; (3) an antifungal compound selected by the method above; (4) killing a fungus; (5) an osmosensing histidine kinase having no transmembrane region and derived from a plant-pathogenic filamentous fungus or which has an amino acid sequence selected from: (a) a sequence of 1293, 1307 or 1438 amino acids (SEQ ID NO: 41, 55 or 68) given in the specification or a sequence 95% or more homologous to SEQ ID NO: 41, 55 or 68; (b) a sequence encoded by a DNA amplified by PCR using a Fusarium oxysporum-derived cDNA as a template and using oligonucleotides having the nucleotide sequences tgcactagtatggttgacgacgcggccctcgc (SEQ ID NO: 52) and gagctgcagttagttggtaagacttcgcatatc (SEQ ID NO: 53) as primers;(c) a sequence encoded by a DNA amplified by PCR using Mycospharella tritici-derived cDNA as a template and using oligonucleotides having the sequences cccactagtatgctgcaagaagagacttcg (SEQ ID NO: 64) and

cctaagcttctcagctgctatgggcacgaa (SEQ ID NO: 65) as primers; (d) a sequence encoded by a DNA amplified by PCR using Thanapethorus cucumeris-derived cDNA as a template and using oligonucleotides having the sequences ggaactagtatggcaggtacaacgggggggacacc (SEQ ID NO: 85) and tgcaagcttttagtgggcaccgtggggtgttacg (SEQ ID NO: 86) as primers; and (e) a sequence derived from Phytophthora infestans and has the amino acid sequence of 124 amino acids (SEQ ID NO: 90) given in the specification; (6) a polynucleotide having a nucleotide sequence encoding an amino acid sequence of an osmosensing histidine kinase having no transmembrane region derived from a plant-pathogen filamentous fungus described above or having a sequence of 3882, 3924, or 4317 bp (SEQ ID NO: 42, 56, or 69) given in the specification; (7) obtaining the polynucleotide above; and (8) an oligonucleotide which comprises a nucleotide sequence selected from 17 sequences of 23-34 bp (SEQ ID NO: 30-40, 52, 53, 64, 65, 85, and 86) given in the specification, e.g., aacatgtcccacgarattcgmacacc (SEQ ID NO: 30) caccgagattcgvacacccatgaaygg (SEQ ID NO: 31) aggccttccaaaaggctctvcggga (SEQ ID NO: 32) gagatggaccctgaaatcacmac (SEQ ID NO: 33) cagatattctcyagygaagtytckcg (SEQ ID NO: 34) atagcrttgccaacmaggttmagaataa (SEQ ID NO: 35) aacttgatggcrttkccaacmaggtt (SEQ ID NO: 36) ctctgtgaacttgatrgcrttkccaac (SEQ ID NO: 37) atacacttttcncggtcacccatcat (SEQ ID NO: 38) tccatctgbgcctggatacacttttc (SEQ ID NO: 39) ggcttvgavagatactcgtccatctg (SEQ ID NO: 40).

BIOTECHNOLOGY - Preferred Transformed Cell: The polynucleotide is a polynucleotide complementing the deficiency in hybrid-sensor kinase in the cell deficient in at least one hybrid-sensor kinase in which the polynucleotide has been introduced. The cell is a microorganism, particularly budding yeast. The osmosensing histidine kinase having no transmembrane region is an osmosensing histidine kinase having no transmembrane region and having a mutation which confers resistance to any of a dicarboxylimide antifungal compound, an aromatic hydrocarbon antifungal compound and a phenylpyrrole antifungal compound to the cell. The osmosensing histidine kinase is derived from a plant -pathogenic filamentous fungus and has no transmembrane region. The osmosensing histidine kinase has an amino acid sequence of 1315, 1307, 1293, 1307, 1438 or 124 amino acids (SEQ ID NO: 1, 16, 41, 55, 68 or 90, respectively) given in the specification. The nucleotide sequence encoding an amino acid sequence of the osmosensing histidine kinase is a sequence of 3948, 3924, 3882, 3924, or 4317 bp (SEQ ID NO: 2, 17, 42, 56, or 69, respectively) also given in the specification. Preferred Method: Assaying the antifungal activity of a substance comprises culturing a transformed cell defined above in the presence of a test substance, measuring an amount of intracellular signal transduction from the osmosensing histidine kinase having no transmembrane region expressed in the cultured transformed cell or an index value having the correlation, and assessing the antifungal activity of the test substance based on a difference between an amount of intracellular signal transduction or an index value having the correlation measured and a control. The amount of intracellular signal transduction or the index value having the correlation is an amount of growth of the transformed cell. Identifying an antifungal compound comprises selecting an antifungal compound based on the antifungal activity assessed in the assaying method defined above. Killing a fungus comprises identifying an antifungal compound by the method above and contacting the fungus with the identified antifungal compound. Obtaining the polynucleotide above comprises amplifying a desired polynucleotide by PCR using the oligonucleotide above and recovering the amplified desired polynucleotide.

ACTIVITY - Fungicide. No biological data given.

MECHANISM OF ACTION - None given.

USE - The transformed cell is useful for assaying the antifungal activity of a substance and identifying an antifungal compound which is

useful for killing a fungus (claimed).

EXAMPLE - BcOS-1 DNA was cloned into a shuttle vector p415ADH (ATCC87312) replicable in yeast and Escherichia coli. Both were digested, separated by agarose gel electrophoresis, and a part of the gel containing a desired DNA was excised. The BcOS-1 DNA was inserted between SpeI and PstI sites in the multicloning site of the shuttle vector. A nucleotide sequence of the resulting expression plasmid was analyzed after a sequencing reaction. The nucleotide sequence of 3948 bp (SEQ ID NO: 2) given in the specification was obtained and it was confirmed that the expression plasmid pADHBcOS1 harbored a DNA having a nucleotide sequence encoding an amino acid sequence of BcOS-1. The prepared expression plasmid was introduced into each of budding yeast (Saccharomyces cerevisiae AH22 strain) (IFO10144) and TM182 strain. By utilizing disappearance of leucine auxotrophy in the resulting transformed budding yeast, the transformed budding yeast AH22 strain was selected on a Glu-Leu agar medium, and the transformed budding yeast TM182 was selected on a Gal-Ura-Leu agar medium. It was confirmed that the resulting TM182-BcOS1 grows even when transplanted to a Glu-Ura-Leu medium. (211 pages)

L8 ANSWER 4 OF 11 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN

ACCESSION NUMBER: 2005:7748 BIOSIS
DOCUMENT NUMBER: PREV200500007354
TITLE: Evolution of an osmosensing histidine kinase in field strains of Botryotinia fuckeliana (Botrytis cinerea) in response to dicarboximide fungicide usage.
AUTHOR(S): Cui, Wei; Beever, Ross E. [Reprint Author]; Parkes, Stephanie L.; Templeton, Matthew D.
CORPORATE SOURCE: Landcare Res, Private Bag 92 170, Auckland, New Zealand BeeverR@LandcareResearch.co.nz
SOURCE: Phytopathology, (October 2004) Vol. 94, No. 10, pp. 1129-1135. print.
ISSN: 0031-949X (ISSN print).
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 16 Dec 2004
Last Updated on STN: 16 Dec 2004

AB DNA sequence polymorphisms in the putative two-component histidine protein kinase encoded by the Daf1 gene have been identified within a sample of 5 sensitive and 27 dicarboximide-resistant field strains of Botryotinia fuckeliana (anamorph Botrytis cinerea). The gene of 3948 by is predicted to encode a 1315-amino acid protein comprising an N-terminal region, an amino acid repeat region, which has been hypothesized to be the binding site for dicarboximide fungicide, and a C-terminal region encompassing kinase and response regulator domains. Two amino acid variants were distinguished among the sensitive strains characterized by alanine (group 1), or threonine (group 2), at position 1259 in the C-terminal region. All resistant strains could be classified into either group 1 or group 2 but, in addition, all showed changes in the second amino acid repeat region. On the basis of the differences in this repeat region, four classes of resistant strains were recognized; class 1 characterized by an isoleucine to serine mutation, class 2 by an isoleucine to asparagine mutation, class 3 by an isoleucine to arginine mutation (all at position 365), and class 4 by an isoleucine to serine mutation (position 365) as well as a glutamine to proline mutation (position 369). All classes showed similar low levels of resistance to iprodione and to vinclozolin, except for class 3 and class 4 strains, which show low resistance to iprodione but moderate (class 3) or high (class 4) resistance to vinclozolin. The classes as a group did not differ from sensitive strains in osmotic sensitivity measured as mycelial growth response, but some class 1 strains showed an abnormal morphology on osmotically amended medium. The evolution of the amino acid differences is discussed in relation to field observations. It is proposed that class 1 and class 2

strains arose by single mutations within the sensitive population, whereas classes 3 and 4 arose by single mutations within a resistant population.

L8 ANSWER 5 OF 11 MEDLINE on STN
ACCESSION NUMBER: 2003280893 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12672798
TITLE: Analysis of the role of the EnvZ linker region in signal transduction using a chimeric Tar/EnvZ receptor protein, Tez1.
AUTHOR: Zhu Yan; Inouye Masayori
CORPORATE SOURCE: Department of Biochemistry, Robert Wood Johnson Medical School, Piscataway, New Jersey 08854, USA.
CONTRACT NUMBER: GM19043 (NIGMS)
SOURCE: The Journal of biological chemistry, (2003 Jun 20) Vol. 278, No. 25, pp. 22812-9. Electronic Publication: 2003-04-02.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE) (RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200308
ENTRY DATE: Entered STN: 17 Jun 2003
Last Updated on STN: 22 Aug 2003
Entered Medline: 21 Aug 2003

AB Tez1 is a chimeric protein in which the periplasmic and transmembrane domains of Tar, a chemosensor, are fused to the cytoplasmic catalytic domain of EnvZ, an osmosensing histidine kinase, through the EnvZ linker. Unlike Taz1 (a similar hybrid with the Tar linker), Tez1 could not respond to Tar ligand, aspartate, whereas single Ala insertion at the transmembrane/linker junction, as seen in Tez1A1, restored the aspartate-regulatable phenotype. Analysis of the Ala insertion site requirement and the nature of the insertion residue on the phenotype of Tez1 indicated that a junction region between the transmembrane domain and the predicted helix I in the linker is critical to signal transduction. Random mutagenesis revealed that P185Q mutation in the Tez1 linker restored the aspartate-regulatable phenotype. Substitution mutations at Pro-185 further demonstrated that specific residues are required at this site for an aspartate response. None of the hybrid receptors constructed with different Tar/EnvZ fusion sites in the linker could respond to aspartate, suggesting that specific interactions between the two predicted helices in the linker are important for the linker function. In addition, a mutation (F220D) known to cause an OmpCc phenotype in EnvZ resulted in similar OmpCc phenotypes in both Tez1A1 and Tez1, indicating the importance of the predicted helix II in signal propagation. Together, we propose that the N-terminal junction region modulates the alignment between the two helices in the linker upon signal input. In turn helix II propagates the resultant conformational signal into the downstream catalytic domain of EnvZ to regulate its bifunctional enzymatic activities.

L8 ANSWER 6 OF 11 MEDLINE on STN
ACCESSION NUMBER: 2003231247 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12754242
TITLE: Cysteine-scanning analysis of the dimerization domain of EnvZ, an osmosensing histidine kinase.
AUTHOR: Qin Ling; Cai Shengjian; Zhu Yan; Inouye Masayori
CORPORATE SOURCE: Department of Biochemistry, UMDNJ-Robert Wood Johnson Medical School, Piscataway, New Jersey 08854, USA.
CONTRACT NUMBER: GM19043 (NIGMS)
SOURCE: Journal of bacteriology, (2003 Jun) Vol. 185, No. 11, pp. 3429-35.

Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE) (RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200306
ENTRY DATE: Entered STN: 20 May 2003
Last Updated on STN: 13 Jun 2003
Entered Medline: 12 Jun 2003

AB EnvZ and OmpR are a transmembrane sensor and its cognate response regulator, respectively, regulating the transcription of porin genes in response to medium osmolarity in Escherichia coli. The cytoplasmic domain of EnvZ (EnvZc) possesses both kinase and phosphatase activities and can be dissected into two functional domains, A and B. Here, we performed a cysteine-scanning analysis of domain A, a 67-residue central dimerization and phosphatase domain containing His-243 as the phosphorylation site, and we examined the effects of the cysteine substitution mutations on the enzymatic activities of domain A. The substitution mutations were made at 31 residues, from which 24 mutant domain A proteins were biochemically characterized. From the analysis of the phosphatase activity of purified mutant proteins, it was found that there are two regions in domain A which are important for this activity. Cysteine mutations in these regions dramatically reduce or completely abolish the phosphatase activity of domain A. The mutations that have the most-severe effects on domain A phosphatase activity also significantly reduce the phosphatase activity of EnvZc containing the same mutation. Using an in vitro complementation system with EnvZc(H243V), these cysteine mutants were further characterized for their autophosphorylation activities as well as their phosphotransfer activities. The results indicate that some mutations are specific either for the phosphatase activity or for the kinase activity.

L8 ANSWER 7 OF 11 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
DUPLICATE 1
ACCESSION NUMBER: 2002:481912 BIOSIS
DOCUMENT NUMBER: PREV200200481912
TITLE: An osmosensing histidine kinase mediates dicarboximide fungicide resistance in Botryotinia fuckeliana (Botrytis cinerea).
AUTHOR(S): Cui, Wei; Beever, Ross E.; Parkes, Stephanie L.; Weeds, Pauline L.; Templeton, Matthew D. [Reprint author]
CORPORATE SOURCE: Plant Health and Development Group, Horticulture and Food Research Institute of New Zealand Ltd., Private Bag 92 169, Auckland, New Zealand
mtempleton@hortresearch.co.nz
SOURCE: Fungal Genetics and Biology, (August, 2002) Vol. 36, No. 3, pp. 187-198. print.
ISSN: 1087-1845.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 11 Sep 2002
Last Updated on STN: 11 Sep 2002

AB A two-component histidine protein kinase gene, homologous to os-1 from Neurospora crassa, was cloned and sequenced from a single ascospore isolate of Botryotinia fuckeliana. A series of nine spontaneous mutants resistant to dicarboximide fungicides was selected from this strain and characterized with respect to fungicide resistance and osmotic sensitivity. Genetic crosses of the mutants with an authentic Daf1 strain showed that the phenotypes mapped to this locus. Single point mutations (seven transitions, one transversion, and one short deletion) were detected in the alleles of the nine mutants sequenced. The mutational changes were shown to cosegregate with the dicarboximide resistance and osmotic sensitivity phenotypes in progeny obtained from crossing selected resistant strains with a sensitive strain. All mutations detected are

predicted to result in amino acid changes in the coiled-coil region of the putative Dafl histidine kinase, and it is proposed that dicarboximide fungicides target this domain.

L8 ANSWER 8 OF 11 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2000223645 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10760160
TITLE: A monomeric histidine kinase derived from EnvZ, an Escherichia coli osmosensor.
AUTHOR: Qin L; Dutta R; Kurokawa H; Ikura M; Inouye M
CORPORATE SOURCE: Department of Biochemistry, UMDNJ, Robert Wood Johnson Medical School, 675 Hoes Lane, Piscataway, NJ 08854, USA.
SOURCE: Molecular microbiology, (2000 Apr) Vol. 36, No. 1, pp. 24-32.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 6 Jun 2000
Last Updated on STN: 6 Jun 2000
Entered Medline: 23 May 2000

AB Histidine kinases function as dimers. The kinase domain of the osmosensing histidine kinase EnvZ of Escherichia coli consists of two domains: domain A (67 residues) responsible for histidine phosphotransfer and dimerization, and domain B (161 residues) responsible for the catalytic and ATP-binding function. The individual structures of these two domains have been recently solved by NMR spectroscopy. Here, we demonstrate that an enzymatically functional monomeric histidine kinase can be constructed by fusing in tandem two domains A and one domain B to produce a single polypeptide (A-A-B). We show that this protein, EnvZc[AAB], is soluble and exists as a stable monomer. The autophosphorylation and OmpR kinase activities of the monomeric EnvZc[AAB] are similar to that of the wild-type EnvZ, while OmpR-binding and phosphatase functions are reduced. V8 protease digestion and mutational analyses indicate that His-243 of only the amino proximal domain A is phosphorylated. Based on these results, molecular models are proposed for the structures of EnvZc[AAB] and the kinase domain of EnvZ. The present results demonstrate for the first time the construction of a functional, monomeric histidine kinase, further structural studies of which may provide important insights into the structure-function relationships of histidine kinases.

L8 ANSWER 9 OF 11 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN DUPLICATE 3
ACCESSION NUMBER: 1999:490710 BIOSIS
DOCUMENT NUMBER: PREV199900490710
TITLE: Osmosensing histidine kinases
AUTHOR(S): Alex, Lisa A. [Inventor, Reprint author]; Simon, Melvin I. [Inventor]; Selitrennikoff, Claude [Inventor]; Agnan, Jacqueline [Inventor]
CORPORATE SOURCE: California Institute of Technology, Pasadena, CA, USA
ASSIGNEE: California Institute of Technology
PATENT INFORMATION: US 5939306 19990817
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Aug. 17, 1999) Vol. 1225, No. 3. print.
CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 16 Nov 1999

Last Updated on STN: 16 Nov 1999

L8 ANSWER 10 OF 11 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 1998154430 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9493379
TITLE: Isolation of CaSLN1 and CaNIK1, the genes for osmosensing histidine kinase homologues, from the pathogenic fungus Candida albicans.
AUTHOR: Nagahashi S; Mio T; Ono N; Yamada-Okabe T; Arisawa M; Bussey H; Yamada-Okabe H
CORPORATE SOURCE: Department of Biology, McGill University, Montreal, Quebec, Canada.
SOURCE: Microbiology (Reading, England), (1998 Feb) Vol. 144 (Pt 2), pp. 425-32.
Journal code: 9430468. ISSN: 1350-0872.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB006362; GENBANK-AB006363
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 30 Apr 1998
Last Updated on STN: 11 Feb 2003
Entered Medline: 21 Apr 1998

AB Recent studies have revealed that fungi possess a mechanism similar to bacterial two-component systems to respond to extracellular changes in osmolarity. In Saccharomyces cerevisiae, Sln1p contains both histidine kinase and receiver (response regulator) domains and acts as an osmosensor protein that regulates the downstream HOG1 MAP kinase cascade. SLN1 of Candida albicans was functionally cloned using an S. cerevisiae strain in which SLN1 expression was conditionally suppressed. Deletion analysis of the cloned gene demonstrated that the receiver domain of C. albicans Sln1p was not necessary to rescue SLN1-deficient S. cerevisiae strains. Unlike S. cerevisiae, a null mutation of C. albicans SLN1 was viable under regular and high osmotic conditions, but it caused a slight growth retardation at high osmolarity. Southern blotting with C. albicans SLN1 revealed the presence of related genes, one of which is highly homologous to the NIK1 gene of Neurospora crassa. Thus, C. albicans harbours both SLN1- and NIK1-type histidine kinases.

L8 ANSWER 11 OF 11 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 97287887 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9142740
TITLE: The osmotic-1 locus of Neurospora crassa encodes a putative histidine kinase similar to osmosensors of bacteria and yeast.
AUTHOR: Schumacher M M; Enderlin C S; Selitrennikoff C P
CORPORATE SOURCE: University of Colorado Health Sciences Center, B-111, 4200 East 9th Avenue, Denver, CO 80262, USA.
CONTRACT NUMBER: R01:AI33354-02 (NIAID)
SOURCE: Current microbiology, (1997 Jun) Vol. 34, No. 6, pp. 340-7.
Journal code: 7808448. ISSN: 0343-8651.
PUB. COUNTRY: United States
DOCUMENT TYPE: (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LANGUAGE: English
FILE SEGMENT: Biotechnology
OTHER SOURCE: GENBANK-U53189
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 16 Jul 1997
Last Updated on STN: 16 Jul 1997
Entered Medline: 30 Jun 1997

AB Osmotically sensitive mutants of Neurospora crassa are unable to grow on medium supplemented with 4% NaCl, have altered morphologies and cell-wall compositions, and are resistant to dicarboximide fungicides. Osmotic-1 (os-1) mutants have a unique characteristic of forming protoplasts that grow and divide in specialized liquid medium, suggesting that the os-1+ gene product is important for cell-wall assembly. A cosmid containing the os-1+ locus of N. crassa, isolated from a genomic cosmid library by chromosomal walk from a closely linked gene, was used to subclone the os-1+ gene by functional complementation of an os-1 mutant. Analysis of the sequence of complementing DNA predicts that os-1+ encodes a predicted protein similar to sensor-histidine kinases of bacteria and a yeast osmosensor-histidine kinase. Importantly, the predicted os-1+ protein is identical to the N. crassa nik-1 predicted protein that was identified by using polymerase chain reaction primers directed against histidine kinase consensus DNA sequences. Our results indicate that nik-1 and os-1 encode the same osmosensing histidine kinase that plays an important role in the regulation of cell-wall assembly and, probably, other cell responses to changes in external osmolarity.

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=> e nakajima h/au
E1            5     NAKAJIMA GORO/AU
E2            1     NAKAJIMA GOZO/AU
E3         9134 --> NAKAJIMA H/AU
E4            4     NAKAJIMA H */AU
E5           18     NAKAJIMA H H/AU
E6           56     NAKAJIMA H O/AU
E7           14     NAKAJIMA HACHIRO/AU
E8           14     NAKAJIMA HADJIME/AU
E9          151     NAKAJIMA HAJIME/AU
E10           1     NAKAJIMA HANAE/AU
E11           5     NAKAJIMA HANAKO/AU
E12           8     NAKAJIMA HARU/AU

=> s e3
L9         9134 "NAKAJIMA H"/AU

=> d hios
'HIOS' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files.  Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):d his
'D' IS NOT A VALID FORMAT
'HIS' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files.  Refer to file specific help messages
or the STNGUIDE file for information on formats available in
individual files.
REENTER DISPLAY FORMAT FOR ALL FILES (FILEDEFAULT):end

=> d his

     (FILE 'HOME' ENTERED AT 15:42:50 ON 02 JUL 2007)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 15:43:53 ON 02 JUL 2007
L1            55 S OSMOSENSING (W) HISTIDINE (W) KINASE?
L2           135 S HYBRID(W)SENSOR (W)KINASE
L3             0 S L2(W)(LACK? OR DEFICIENT? OR MISS?)
L4             2 S L1 AND L2
L5            12 S CELL AND L1
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L6             6 DUP REM L5 (6 DUPLICATES REMOVED)
L7            25 S (PLANT? OR BACTER?) AND L1
L8            11 DUP REM L7 (14 DUPLICATES REMOVED)
                 E NAKAJIMA H/AU
L9          9134 S E3

=> s l1 and l9
L10            1 L1 AND L9

=> d ibib ab

L10   ANSWER 1 OF 1  BIOTECHDS COPYRIGHT 2007 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2004-15129  BIOTECHDS
TITLE:            New transformed cell in which a polynucleotide coding for
                  osmosensing histidine kinase
                  having no transmembrane region has been introduced, useful
                  for identifying an antifungal compound useful for killing a
                  fungus;
                     vector expression in host cell for use in drug screening
                     and fungus infection therapy
AUTHOR:           NAKAJIMA H
PATENT ASSIGNEE:  SUMITOMO CHEM CO LTD
PATENT INFO:      EP 1415996 6 May 2004
APPLICATION INFO: EP 2003-256895 30 Oct 2003
PRIORITY INFO:    JP 2002-317736 31 Oct 2002; JP 2002-317736 31 Oct 2002
DOCUMENT TYPE:    Patent
LANGUAGE:         English
OTHER SOURCE:     WPI: 2004-341880 [32]
AB    DERWENT ABSTRACT:
      NOVELTY - A transformed cell in which a polynucleotide having a sequence
      encoding an amino acid sequence of an osmosensing
      histidine kinase having no transmembrane region has
      been introduced in a functional form into a cell deficient in at least
      one hybrid-sensor kinase, is new.
           DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for: (1)
      assaying the antifungal activity of a substance; (2) identifying an
      antifungal compound; (3) an antifungal compound selected by the method
      above; (4) killing a fungus; (5) an osmosensing
      histidine kinase having no transmembrane region and
      derived from a plant-pathogenic filamentous fungus or which has an amino
      acid sequence selected from: (a) a sequence of 1293, 1307 or 1438 amino
      acids (SEQ ID NO: 41, 55 or 68) given in the specification or a sequence
      95% or more homologous to SEQ ID NO: 41, 55 or 68; (b) a sequence encoded
      by a DNA amplified by PCR using a Fusarium oxysporum-derived cDNA as a
      template and using oligonucleotides having the nucleotide sequences
      tgcactagtatggttgacgacgcggccctcgc (SEQ ID NO: 52) and
      gagctgcagttagttggtaagacttcgcatatc (SEQ ID NO: 53) as primers;(c) a
      sequence encoded by a DNA amplified by PCR using Mycospharella
      tritici-derived cDNA as a template and using oligonucleotides having the
      sequences cccactagtatgctgcaagaagagacttcg (SEQ ID NO: 64) and
      cctaagcttctcagctgctatgggcacgaa (SEQ ID NO: 65) as primers; (d) a sequence
      encoded by a DNA amplified by PCR using Thanapethorus cucumeris-derived
      cDNA as a template and using oligonucleotides having the sequences
      ggaactagtatggcaggtacaacgggggacacc (SEQ ID NO: 85) and
      tgcaagcttttagtgggcaccgtggggtgttacg (SEQ ID NO: 86) as primers; and (e) a
      sequence derived from Phytophthora infestans and has the amino acid
      sequence of 124 amino acids (SEQ ID NO: 90) given in the specification;
      (6) a polynucleotide having a nucleotide sequence encoding an amino acid
      sequence of an osmosensing histidine kinase
      having no transmembrane region derived from a plant-pathogen filamentous
      fungus described above or having a sequence of 3882, 3924, or 4317 bp
      (SEQ ID NO: 42, 56, or 69) given in the specification; (7) obtaining the
      polynucleotide above; and (8) an oligonucleotide which comprises a
      nucleotide sequence selected from 17 sequences of 23-34 bp (SEQ ID NO:
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30-40, 52, 53, 64, 65, 85, and 86) given in the specification, e.g., aacatgtcccacgarattcgmacacc (SEQ ID NO: 30) caccgagattcgvacacccatgaaygg (SEQ ID NO: 31) aggccttccaaaaggctctvcggga (SEQ ID NO: 32) gagatggaccctgaaatcacmac (SEQ ID NO: 33) cagatattctcyagygaagtytckcg (SEQ ID NO: 34) atagcrttgccaacmaggttmagaataa (SEQ ID NO: 35) aacttgatggcrttkccaacmaggtt (SEQ ID NO: 36) ctctgtgaacttgatrgcrttkccaac (SEQ ID NO: 37) atacacttttcncggtcacccatcat (SEQ ID NO: 38) tccatctgbgcctggatacacttttc (SEQ ID NO: 39) ggcttvgavagatactcgtccatctg (SEQ ID NO: 40).

BIOTECHNOLOGY - Preferred Transformed Cell: The polynucleotide is a polynucleotide complementing the deficiency in hybrid-sensor kinase in the cell deficient in at least one hybrid-sensor kinase in which the polynucleotide has been introduced. The cell is a microorganism, particularly budding yeast. The osmosensing histidine kinase having no transmembrane region is an osmosensing histidine kinase having no transmembrane region and having a mutation which confers resistance to any of a dicarboxylimide antifungal compound, an aromatic hydrocarbon antifungal compound and a phenylpyrrole antifungal compound to the cell. The osmosensing histidine kinase is derived from a plant-pathogenic filamentous fungus and has no transmembrane region. The osmosensing histidine kinase has an amino acid sequence of 1315, 1307, 1293, 1307, 1438 or 124 amino acids (SEQ ID NO: 1, 16, 41, 55, 68 or 90, respectively) given in the specification. The nucleotide sequence encoding an amino acid sequence of the osmosensing histidine kinase is a sequence of 3948, 3924, 3882, 3924, or 4317 bp (SEQ ID NO: 2, 17, 42, 56, or 69, respectively) also given in the specification. Preferred Method: Assaying the antifungal activity of a substance comprises culturing a transformed cell defined above in the presence of a test substance, measuring an amount of intracellular signal transduction from the osmosensing histidine kinase having no transmembrane region expressed in the cultured transformed cell or an index value having the correlation, and assessing the antifungal activity of the test substance based on a difference between an amount of intracellular signal transduction or an index value having the correlation measured and a control. The amount of intracellular signal transduction or the index value having the correlation is an amount of growth of the transformed cell. Identifying an antifungal compound comprises selecting an antifungal compound based on the antifungal activity assessed in the assaying method defined above. Killing a fungus comprises identifying an antifungal compound by the method above and contacting the fungus with the identified antifungal compound. Obtaining the polynucleotide above comprises amplifying a desired polynucleotide by PCR using the oligonucleotide above and recovering the amplified desired polynucleotide.

ACTIVITY - Fungicide. No biological data given.

MECHANISM OF ACTION - None given.

USE - The transformed cell is useful for assaying the antifungal activity of a substance and identifying an antifungal compound which is useful for killing a fungus (claimed).

EXAMPLE - BcOS-1 DNA was cloned into a shuttle vector p415ADH (ATCC87312) replicable in yeast and Escherichia coli. Both were digested, separated by agarose gel electrophoresis, and a part of the gel containing a desired DNA was excised. The BcOS-1 DNA was inserted between SpeI and PstI sites in the multicloning site of the shuttle vector. A nucleotide sequence of the resulting expression plasmid was analyzed after a sequencing reaction. The nucleotide sequence of 3948 bp (SEQ ID NO: 2) given in the specification was obtained and it was confirmed that the expression plasmid pADHBcOS1 harbored a DNA having a nucleotide sequence encoding an amino acid sequence of BcOS-1. The prepared expression plasmid was introduced into each of budding yeast (Saccharomyces cerevisiae AH22 strain) (IFO10144) and TM182 strain. By utilizing disappearance of leucine auxotrophy in the resulting

transformed budding yeast, the transformed budding yeast AH22 strain was selected on a Glu-Leu agar medium, and the transformed budding yeast TM182 was selected on a Gal-Ura-Leu agar medium. It was confirmed that the resulting TM182-BcOS1 grows even when transplanted to a Glu-Ura-Leu medium. (211 pages)

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=> d his

     (FILE 'HOME' ENTERED AT 15:42:50 ON 02 JUL 2007)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 15:43:53 ON 02 JUL 2007
L1            55 S OSMOSENSING (W) HISTIDINE (W) KINASE?
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L3             0 S L2(W)(LACK? OR DEFICIENT? OR MISS?)
L4             2 S L1 AND L2
L5            12 S CELL AND L1
L6             6 DUP REM L5 (6 DUPLICATES REMOVED)
L7            25 S (PLANT? OR BACTER?) AND L1
L8            11 DUP REM L7 (14 DUPLICATES REMOVED)
                 E NAKAJIMA H/AU
L9          9134 S E3
L10            1 S L1 AND L9
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	Document ID	Kind Codes	Source	Issue Date	Pages	Title
1	US 20060269951 A1		US-PGPUB	20061130	114	Inhibitors of autoinducer transporters
2	US 20060057607 A1		US-PGPUB	20060316	37	Small RNAs and bacterial strains involved in quorum sensing
3	US 20040137594 A1		US-PGPUB	20040715	37	Transformed cell with enhanced sensitivity to antifungal compound and use thereof
4	US 20030165932 A1		US-PGPUB	20030904	113	Inhibitors of autoinducer transporters
5	US 7183099 B2		USPAT	20070227	106	Inhibitors of autoinducer transporters

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
1	US 20070141578 A1		US-PGPUB	20070621	31	LuxO-sigma54 interactions and methods of use
2	US 20060269951 A1		US-PGPUB	20061130	114	Inhibitors of autoinducer transporters
3	US 20060057607 A1		US-PGPUB	20060316	37	Small RNAs and bacterial strains involved in quorum sensing
4	US 20040137594 A1		US-PGPUB	20040715	37	Transformed cell with enhanced sensitivity to antifungal compound and use thereof
5	US 20030175930 A1		US-PGPUB	20030918	55	Crystals of LuxP and complexes thereof
6	US 20030165932 A1		US-PGPUB	20030904	113	Inhibitors of autoinducer transporters
7	US 20030023032 A1		US-PGPUB	20030130	32	LuxO-sigma54 interactions and methods of use
8	US 7208612 B2		USPAT	20070424	53	Crystals of LuxP and complexes thereof
9	US 7183099 B2		USPAT	20070227	106	Inhibitors of autoinducer transporters

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
1	US 20070111290 A1		US-PGPUB	20070517	80	Corynebacterium glutamicum genes encoding phosphoenolpyruvate: sugar phosphotransferase system proteins
2	US 20070105167 A1		US-PGPUB	20070510	161	Virulence Associated Nucleic Acid Sequences and Uses Thereof
3	US 20070105122 A1		US-PGPUB	20070510	1202	Primers for synthesizing full-length cDNA and their use
4	US 20070087013 A1		US-PGPUB	20070419	25	Orally-administered live bacterial vaccines for plague
5	US 20070059809 A1		US-PGPUB	20070315	52	Corynebacterium glutamicum genes encoding regulatory proteins
6	US 20070022495 A1		US-PGPUB	20070125	52	Transcription factors for increasing yield
7	US 20070015252 A1		US-PGPUB	20070118	57	Corynebacterium glutamicum genes encoding regulatory proteins
8	US 20070015251 A1		US-PGPUB	20070118	80	Corynebacterium glutamicum genes encoding phosphoenolpyruvate: sugar phosphotransferase system proteins
9	US 20070015168 A1		US-PGPUB	20070118	127	Methods for monitoring multiple gene expression
10	US 20060292674 A1		US-PGPUB	20061228	81	Corynebacterium glutamicum genes encoding phosphoenolpyruvate: sugar phosphotransferase system proteins

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
11	US 20060269951 A1		US-PGPUB	20061130	114	Inhibitors of autoinducer transporters
12	US 20060194285 A1		US-PGPUB	20060831	24	Biological production of clavulanic acid and related compounds
13	US 20060172395 A1		US-PGPUB	20060803	39	Polynucleotides for production of farnesyl dibenzodiazepinones
14	US 20060141583 A1		US-PGPUB	20060629	173	Elaiophylin biosynthetic gene cluster
15	US 20060057607 A1		US-PGPUB	20060316	37	Small RNAs and bacterial strains involved in quorum sensing
16	US 20050287641 A1		US-PGPUB	20051229	168	Gene encoding a nonribosomal peptide synthetase for the production of ramoplanin
17	US 20050287169 A1		US-PGPUB	20051229	23	Methods of use of genes of pyridoxal 5'-phosphate biosynthesis in Bacillus subtilis: avirulent strains for vaccines, and methods for identification of antibacterial agents
18	US 20050260652 A1		US-PGPUB	20051124	134	Compositions and methods that modulate RNA interference
19	US 20050227917 A1		US-PGPUB	20051013	407	Gene products differentially expressed in cancerous cells and their methods of use II
20	US 20050202424 A1		US-PGPUB	20050915	144	Regulators of biofilm formation and uses thereof

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
21	US 20050191733 A1		US-PGPUB	20050901	87	Corynebacterium glutamicum genes encoding phosphoenolpyruvate: sugar phosphotransferase system proteins
22	US 20050176653 A1		US-PGPUB	20050811	248	Polyene polyketides and methods of production
23	US 20050153402 A1		US-PGPUB	20050714	65	Corynebacterium glutamicum genes encoding regulatory proteins
24	US 20050147999 A1		US-PGPUB	20050707	75	Lyme disease vaccines
25	US 20050112664 A1		US-PGPUB	20050526	15	Nucleotide sequences coding for the citA gene
26	US 20050070698 A1		US-PGPUB	20050331	41	Macrolide efflux genetic assembly
27	US 20050043297 A1		US-PGPUB	20050224	195	Farnesyl dibenzodiazepinone, processes for its production and its use as a pharmaceutical
28	US 20050014234 A1		US-PGPUB	20050120	114	Genes from the corynebacterium glutamicum coding for regulatory proteins
29	US 20040265313 A1		US-PGPUB	20041230	15	Methods to regulate biofilm formation
30	US 20040248264 A1		US-PGPUB	20041209	26	Genes coding for phosphoenopyruvate-sugar-phosphotransferase proteins
31	US 20040171517 A1		US-PGPUB	20040902	23	Compounds and methods for modulating bacterial functions

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
32	US 20040166553 A1		US-PGPUB	20040826	132	Caged sensors, regulators and compounds and uses thereof
33	US 20040137594 A1		US-PGPUB	20040715	37	Transformed cell with enhanced sensitivity to antifungal compound and use thereof
34	US 20040086913 A1		US-PGPUB	20040506	179	Human genes and gene expression products XVI
35	US 20040053248 A1		US-PGPUB	20040318	243	Novel nucleic acids and polypeptides
36	US 20040009474 A1		US-PGPUB	20040115	195	Novel human polynucleotides and polypeptides encoded thereby
37	US 20030188344 A1		US-PGPUB	20031002	66	Compositions and methods for agrobacterium transformation of plants
38	US 20030165932 A1		US-PGPUB	20030904	113	Inhibitors of autoinducer transporters
39	US 20030157551 A1		US-PGPUB	20030821	21	Nucleotide sequences coding for the MtrA and/or MtrB proteins
40	US 20030148414 A1		US-PGPUB	20030807	58	COMPOSITIONS AND METHODS FOR REGULATING BACTERIAL PATHOGENESIS
41	US 20030134302 A1		US-PGPUB	20030717	102	Libraries of expressible gene sequences
42	US 20030073163 A1		US-PGPUB	20030417	102	Libraries of expressible gene sequences
43	US 20030023075 A1		US-PGPUB	20030130	33	Novel sequences of E. coli O157

44	US 20030022349 A1		US-PGPUB	20030130	165	Virulence-associated nucleic acid sequences and uses thereof

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
45	US 20020164747 A1		US-PGPUB	20021107	141	Gene cluster for ramoplanin biosynthesis
46	US 20020137073 A1		US-PGPUB	20020926	21	Nucleotide sequences coding for the MtrA and/or MtrB proteins
47	US 20020107364 A1		US-PGPUB	20020808	57	Compositions and methods for regulating bacterial pathogenesis
48	US 20020055114 A1		US-PGPUB	20020509	15	Nucleotide sequences coding for the chrS protein
49	US 7205144 B2		USPAT	20070417	14	Nucleotide sequences encoding a sensor kinase, citA, from Corynebacterium glutamicum
50	US 7186513 B2		USPAT	20070306	262	Methods for monitoring multiple gene expression
51	US 7183099 B2		USPAT	20070227	106	Inhibitors of autoinducer transporters
52	US 7141418 B2		USPAT	20061128	77	Streptococcus pneumoniae polynucleotides and sequences
53	US 7101872 B2		USPAT	20060905	160	Farnesyl dibenzodiazepinone, and processes for its production
54	US 7090973 B1		USPAT	20060815	885	Nucleic acid sequences relating to Bacteroides fragilis for diagnostics and therapeutics
55	US 7078185 B2		USPAT	20060718	137	Gene encoding a nonribosomal peptide synthetase for the production of ramoplanin

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
56	US 7060458 B1		USPAT	20060613	588	Nucleic acid and amino acid sequences relating to Staphylococcus epidermidis for diagnostics and therapeutics
57	US 7018794 B2		USPAT	20060328	121	Methods for monitoring multiple gene expression
58	US 6902893 B1		USPAT	20050607	163	Lyme disease vaccines
59	US 6902887 B1		USPAT	20050607	264	Methods for monitoring multiple gene expression
60	US 6884614 B1		USPAT	20050426	84	Corynebacterium glutamicum genes encoding phosphoenolpyruvate: sugar phosphotransferase system proteins
61	US 6855814 B2		USPAT	20050215	31	Sequences of E. coli O157
62	US 6746854 B2		USPAT	20040608	13	Nucleotide sequences encoding histidine kinase from corynebacterium glutamicum
63	US 6734002 B2		USPAT	20040511	14	Nucleotide sequences coding for the chrS protein
64	US 6562958 B1		USPAT	20030513	328	Nucleic acid and amino acid sequences relating to Acinetobacter baumannii for diagnostics and therapeutics
65	US 6551795 B1		USPAT	20030422	455	Nucleic acid and amino acid sequences relating to pseudomonas aeruginosa for diagnostics and therapeutics

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
66	US 6544772 B1		USPAT	20030408	21	Polynucleotides, materials incorporating them, and methods for using them
67	US 6433154 B1		USPAT	20020813	16	Functional receptor/kinase chimera in yeast cells
68	US 6365723 B1		USPAT	20020402	26	Sequences of E. coli O157
69	US 6355411 B1		USPAT	20020312	160	Virulence-associated nucleic acid sequences and uses thereof
70	US 6162627 A		USPAT	20001219	117	Methods of identifying inhibitors of sensor histidine kinases through rational drug design
71	US 6077682 A		USPAT	20000620	126	Methods of identifying inhibitors of sensor histidine kinases through rational drug design
72	US 6043045 A		USPAT	20000328	24	Screening methods for the identification of novel antibiotics
73	US 6020121 A		USPAT	20000201	42	Inhibitors of regulatory pathways
74	US 5955348 A		USPAT	19990921	33	Genetically modified pseudomonas strains with enhanced biocontrol activity
75	US 5876987 A		USPAT	19990302	30	Method, DNA and bacteria for hyperproduction of an antibiotic due to disruption of an AbsA gene

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
76	US 5834278 A		USPAT	19981110	30	Bacterial peptide methionine sulfoxide reductase an adhesion-associated protein, and antibiotic therapies based thereon
77	US 5798243 A		USPAT	19980825	30	Bacterial peptide methionine sulfoxide reductase, and adhesion-associated protein, and antibiotic therapies based thereon
78	US 5756087 A		USPAT	19980526	35	Genetically modified Pseudomonas strains with enhanced biocontrol activity
79	US 5747276 A		USPAT	19980505	20	Screening methods for the identification of novel antibiotics

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
1	US 20040137594 A1		US-PGPUB	20040715	37	Transformed cell with enhanced sensitivity to antifungal compound and use thereof

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
1	US 20070122881 A1		US-PGPUB	20070531	440	Rhamnose-inducible expression systems and methods
2	US 20070077553 A1		US-PGPUB	20070405	1253	BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VACCINIA REGULATORY GENES AND USES THEREOF
3	US 20070031823 A1		US-PGPUB	20070208	625	BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VACCINIA REGULATORY GENES AND USES THEREOF
4	US 20050063994 A1		US-PGPUB	20050324	117	Methods and reagents for decreasing clinical reaction to allergy
5	US 20040152066 A1		US-PGPUB	20040805	46	Freeze-tolerant eukaryotic cells
6	US 20040142357 A1		US-PGPUB	20040722	74	Novel telomerase inhibitors and uses therefor
7	US 20040137594 A1		US-PGPUB	20040715	37	Transformed cell with enhanced sensitivity to antifungal compound and use thereof
8	US 20040086920 A1		US-PGPUB	20040506	62	STARS - a muscle-specific actin-binding protein
9	US 20040048264 A1		US-PGPUB	20040311	82	Methods and compositions for determining gene function
10	US 20040029158 A1		US-PGPUB	20040212	47	HOP - a novel cardiac-restricted transcriptional factor potentially useful for cardiac regeneration and specification
11	US 20040005700 A1		US-PGPUB	20040108	241	Poroplasts

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
12	US 20030233670 A1		US-PGPUB	20031218	144	Gene sequences and uses thereof in plants
13	US 20030232335 A1		US-PGPUB	20031218	240	Minicell-based screening for compounds and proteins that modulate the activity of signalling proteins
14	US 20030224444 A1		US-PGPUB	20031204	240	Antibodies to native conformations of membrane proteins
15	US 20030224369 A1		US-PGPUB	20031204	238	Reverse screening and target identification with minicells
16	US 20030219888 A1		US-PGPUB	20031127	242	Minicell-based bioremediation
17	US 20030219408 A1		US-PGPUB	20031127	242	Methods of making pharmaceutical compositions with minicells
18	US 20030211599 A1		US-PGPUB	20031113	243	Minicell-based delivery agents
19	US 20030211086 A1		US-PGPUB	20031113	239	Minicell-based selective absorption
20	US 20030207833 A1		US-PGPUB	20031106	243	Pharmaceutical compositions with minicells
21	US 20030203481 A1		US-PGPUB	20031030	242	Conjugated minicells
22	US 20030203411 A1		US-PGPUB	20031030	243	Methods of minicell-based delivery
23	US 20030202937 A1		US-PGPUB	20031030	242	Minicell-based diagnostics
24	US 20030199089 A1		US-PGPUB	20031023	243	Membrane to membrane delivery

25	US 20030199088 A1		US-PGPUB	20031023	149	Minicell-based gene therapy

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
26	US 20030199005 A1		US-PGPUB	20031023	243	Solid supports with minicells
27	US 20030198996 A1		US-PGPUB	20031023	240	Minicell libraries
28	US 20030198995 A1		US-PGPUB	20031023	242	Forward screening with minicells
29	US 20030194798 A1		US-PGPUB	20031016	243	Minicell compositions and methods
30	US 20030194714 A1		US-PGPUB	20031016	244	Minicell-based transformation
31	US 20030190749 A1		US-PGPUB	20031009	242	Minicell-producing parent cells
32	US 20030190683 A1		US-PGPUB	20031009	242	Minicell-based rational drug design
33	US 20030190601 A1		US-PGPUB	20031009	242	Target display on minicells
34	US 20030166279 A1		US-PGPUB	20030904	242	Minicell-based transfection
35	US 20030166099 A1		US-PGPUB	20030904	241	Minicells comprising membrane proteins
36	US 20030133971 A1		US-PGPUB	20030717	72	Senescent cell-derived inhibitors of DNA synthesis
37	US 20030077810 A1		US-PGPUB	20030424	68	CHAMP - a novel cardiac helicase-like factor
38	US 20030036079 A1		US-PGPUB	20030220	52	Gene expression alterations underlying the retardation of aging by caloric restriction in mammals

	Document ID	Kind Codes	Source	Issue Date	Pages	Title
39	US 7183105 B2		USPAT	20070227	291	Eubacterial minicells and their use as vectors for nucleic acid delivery and expression
40	US 7160720 B2		USPAT	20070109	62	CHAMP--a novel cardiac helicase-like factor
41	US 7109315 B2		USPAT	20060919	86	Renilla reniformis fluorescent proteins, nucleic acids encoding the fluorescent proteins and the use thereof in diagnostics, high throughput screening and novelty items
42	US 7070957 B2		USPAT	20060704	56	STARS--a muscle-specific actin-binding protein
43	US 6818215 B2		USPAT	20041116	69	Antibodies to senescent cell-derived inhibiters of DNA synthesis
44	US 6521412 B1		USPAT	20030218	71	HsReq*1 and hsReq*2proteins and use thereof to detect CDK2
45	US 6436682 B1		USPAT	20020820	101	Luciferases, fluorescent proteins, nucleic acids encoding the luciferases and fluorescent proteins and the use thereof in diagnostics, high throughput screening and novelty items
46	US 6372249 B1		USPAT	20020416	69	Senscent cell-derived inhibitors of DNA synthesis

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47	US 6232107 B1		USPAT	20010515	104	Luciferases, fluorescent proteins, nucleic acids encoding the luciferases and fluorescent proteins and the use thereof in diagnostics, high throughput screening and novelty items
48	US 5986055 A		USPAT	19991116	69	CDK2 interactions

	L #	Hits	Search Text
1	L1	1	"5939306".pn.
2	L2	9	hybrid adj sensor adj kinase$2
3	L3	140	sensor adj kinase$2
4	L4	0	sensor adj kinase$2 adj (lack? or deficien? or miss?)
5	L5	0	sensor adj kinase adj deficient
6	L6	0	sensor adj kinase adj deficiency
7	L8	5	l2 and l7
8	L7	79	l3 and complement
9	L9	22486	NAKAJIMA
10	L10	15943	transformed adj cell
11	L11	4	l2 and l10
12	L12	1	l9 and l11
13	L13	1162	budding adj yeast$2
14	L15	1	l3 and l14
15	L14	48	l9 and l13